

Supplemental Material

A DNA-DNA hybridisation study of strains of the Flavobacteriaceae family from mostly human clinical sources and proposals of *Chryseobacterium bernardetii* sp. nov., *Chryseobacterium carnis* sp. nov., *Chryseobacterium lactis* sp. nov., *Chryseobacterium nakagawai* sp. nov., and *Chryseobacterium taklimakanense* comb. nov.

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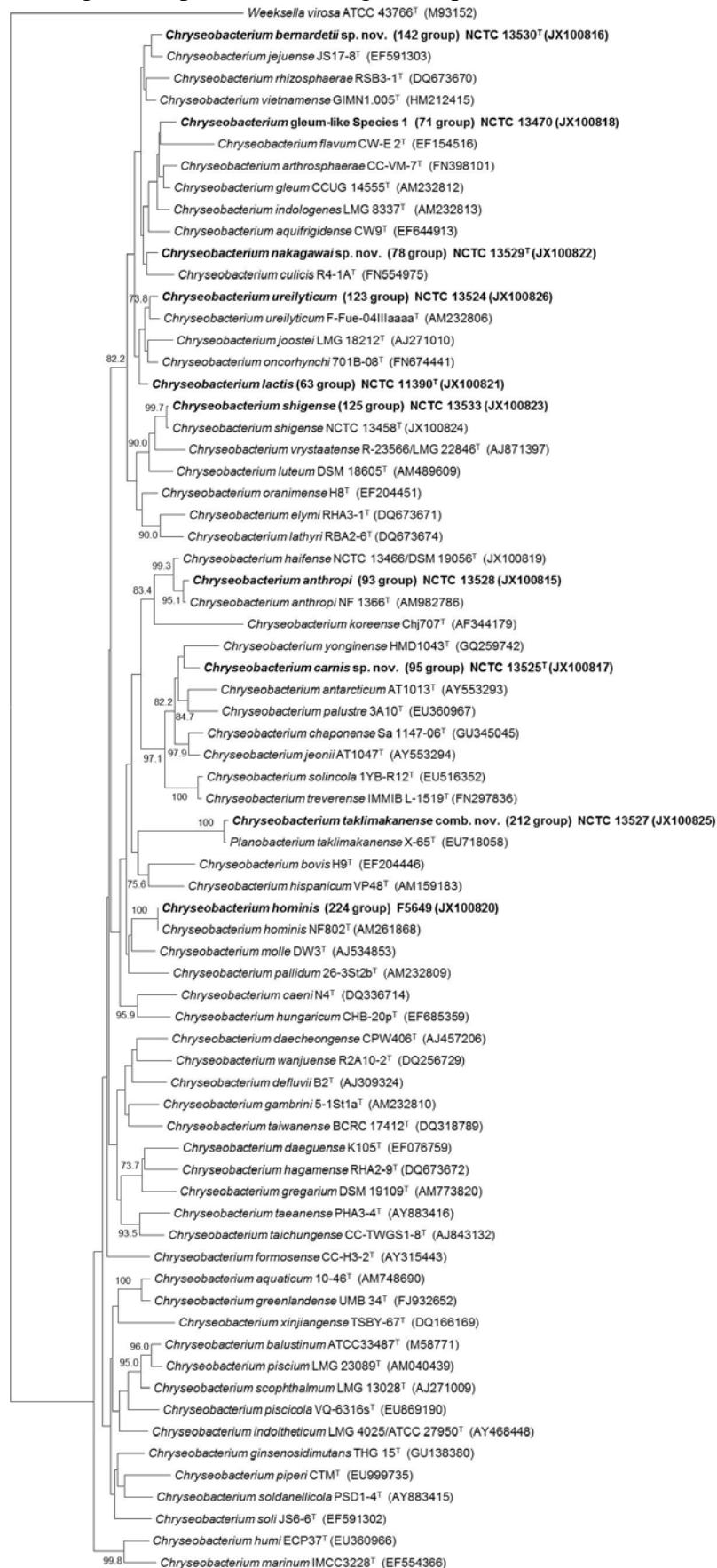
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Table S1: Sequences of primers used for sequencing the 16S rRNA gene.

Name	Sequence
fD1-5p	CCGAATTCGTCGACAACAG
fD1	AGAGTTTGATCMTGGCTCAG
F785	GGATTAGATACCCTGGTA
R357	CTGCTGCCTCCCGTA
R802	TACCAGGGTATCTAATCC
F357	TACGGGAGGCAGCAG
R530	GTATTACCGCGGCTGCTG
R519	GWATTACCGCGGCKGCTG
F530	CAGCAGCCGCGGTAATAC
BSF917	GAATTGACGGGGRCCC
BSR926	CCGTCAATTYYTTTRAGTTT
BSF1099	GYAACGAGCGCAACCC
BSR1114	GGTTGCGCTCGTTRC
BSF1391	TGTACACACCGCCCGTC
BSR1407	GACGGGCGGTGTGTRC
rP2-5p	CCCGGGATCCAAGCTTAC

Figure S1: A rooted Neighbour-joining phylogenetic tree showing the relationships between type strains of all *Chryseobacterium* species using 1336 bp of 16S rRNA gene sequence with *Weeksellia virosa* as the outgroup.



0.005